# An expanded genome-wide association study of type 2 diabetes in Europeans

Running title: **European T2D genome-wide association study**

Robert A Scott[1*], Laura J Scott[2*], Reedik Mägi[3*], Letizia Marullo[4*], Kyle J Gaulton[5-6*], Marika Kaakinen[7*], Natalia Pervjakova[3], Tune H Pers[8-11], Andrew D Johnson[12], John D Eicher[12], Anne U Jackson[2], Teresa Ferreira[5], Yeji Lee[2], Clement Ma[2], Valgerdur Steinthorsdottir[13], Gudmar Thorleifsson[13], Lu Qi[14-16], Natalie R Van Zuydam[5,17], Anubha Mahajan[5], Han Chen[18-19], Peter Almgren[20], Ben F Voight[21-23], Harald Grallert[24-26], Martina Müller-Nurasyid[27-30], Janina S Ried[27], N William Rayner[5,31-32], Neil Robertson[5,31], Lennart C Karssen[33-34], Elisabeth M van Leeuwen[33], Sara M Willems[35], Christian Fuchsberger[2], Phoenix Kwan[2], Tanya M Teslovich[2], Pritam Chanda[36], Man Li [37], Yingchang Lu[38-39], Christian Dina[40-43], Dorothee Thuillier[44-45], Loic Yengo[44-45], Longda Jiang[7], Thomas Sparso[10], Hans Kestler[46-47], Himanshu Chheda[48], Lewin Eisele[49], Stefan Gustafsson[50], Mattias Frånberg[51-53], Rona J Strawbridge[51], Rafn Benediktsson[54-55], Astradur B Hreidarsson[55], Augustine Kong[13], Gunnar Sigurðsson[55-56], Nicola D Kerrison[1], Jian'an Luan[1], Liming Liang[14,57], Thomas Meitinger[58], Michael Roden[59-61], Barbara Thorand[25-26], Tõnu Esko[3,62-63], Evelin Mihailov[3], Caroline Fox[64-65], Ching-Ti Liu[18], Denis Rybin[66], Bo Isomaa[67-68], Valeriya Lyssenko[20], Tiinamaija Tuomi[67,69], David J Couper[70], James S Pankow[71], Niels Grarup[10], Christian T Have[10], Marit E Jørgensen[72], Torben Jørgensen[73-75], Allan Linneberg[73,76-77], Marilyn C Cornelis[78], Rob M van Dam[15,79], David J Hunter[14-15,80-81], Peter Kraft[14,57,81], Qi Sun[15,80], Sarah Edkins[32], Katharine R Owen[31,82], John RB Perry[1], Andrew R Wood[83], Eleftheria Zeggini[32], Juan Tajes-Fernandes[5], Goncalo R Abecasis[2], Lori L Bonnycastle[84], Peter S Chines[84], Heather M Stringham[2], Heikki A Koistinen[85-87], Leena Kinnunen[85-87], Bengt Sennblad[51-52], Thomas W Mühleisen[88-89], Markus M Nöthen[88-89], Sonali Pechlivanis[49], Damiano Baldassarre[90-91], Karl Gertow[51], Steve E Humphries[92], Elena Tremoli[90-91], Norman Klopp[93-94], Julia Meyer[95], Gerald Steinbach[96], Roman Wennauer[97], Johan G Eriksson[98-101], Satu Männistö[98], Leena Peltonen[32,48,98,102,159], Emmi Tikkanen[48,103], Guillaume Charpentier[104], Elodie Eury[45], Stéphane Lobbens[45], Bruna Gigante[105], Karin Leander[105], Olga McLeod[51], Erwin P Bottinger[38], Omri Gottesman[38], Douglas Ruderfer[106], Matthias Blüher[107-108], Peter Kovacs[107-108], Anke Tonjes[107-108], Nisa M Maruthur[37,109-110], Chiara Scapoli[4], Raimund Erbel[49], Karl-Heinz Jöckel[49], Susanne Moebus[49], Ulf de Faire[105], Anders Hamsten[51], Michael Stumvoll[107-108], Panagiotis Deloukas[32,111], Peter J Donnelly[5,112], Timothy M Frayling[83], Andrew T Hattersley[113], Samuli Ripatti[32,48,103,114], Veikko Salomaa[85], Nancy L Pedersen[115], Bernhard O Boehm[116-118], Richard N Bergman[119], Francis S Collins[84], Karen L Mohlke[120], Jaakko Tuomilehto[98,121-123], Torben Hansen[10,124], Oluf Pedersen[10], Inês Barroso[32,125], Lars Lannfelt[126], Erik Ingelsson[50,127], Lars Lind[128], Cecilia M Lindgren[5,102], Stephane Cauchi[44], Philippe Froguel[44-45,129], Ruth JF Loos[38-39,130], Beverley Balkau[131-132], Heiner Boeing[133], Paul W Franks[134-135], Aurelio Barricarte Gurrea[136-138], Domenico Palli[139], Yvonne T van der Schouw[140], David Altshuler[141-146], Leif C Groop[20,147], Claudia Langenberg[1], Nicholas J Wareham[1], Eric Sijbrands[97], Cornelia M van Duijn[33,148], Jose C Florez[63,149-150], James B Meigs[8,150-151], Eric Boerwinkle[152-153], Christian Gieger[24-25], Konstantin Strauch[27,29], Andres Metspalu[3,154], Andrew D Morris[155], Colin NA Palmer[17,156], Frank B Hu[14-16], Unnur Thorsteinsdottir[13,54], Kari Stefansson[13,54], Josée Dupuis[18,64], Andrew P Morris[3,5,157-158#], Michael Boehnke[2#], Mark I McCarthy[5,31,82#], Inga Prokopenko[5,31,129#] for the DIAbetes Genetics Replication And Meta-analysis (DIAGRAM) Consortium.

## Affiliations

1)MRC Epidemiology Unit, University of Cambridge, Cambridge, United Kingdom; 2)Department of Biostatistics and Center for Statistical Genetics, University of Michigan, Ann Arbor, MI, USA; 3)Estonian Genome Center, University of Tartu, Tartu, Estonia; 4)Department of Life Sciences and Biotechnology, University of Ferrara, Ferrara, Italy; 5)Wellcome Trust Centre for Human Genetics, University of Oxford, Oxford, UK; 6)Department of Genetics, Stanford University, Stanford, CA, USA; 7)Department of Genomics of Common Disease, Imperial College London, Du Cane Road, London W12 0NN, United Kingdom; 8)Medical and Population Genetics Program, Broad Institute of MIT and Harvard, Cambridge, 02142, USA; 9)Division of Endocrinology and Center for Basic and Translational Obesity Research, Boston Children's Hospital, Boston, 02115, USA; 10)The Novo Nordisk Foundation Center for Basic Metabolic Research, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark; 11)Department of Epidemiology Research, Statens Serum Institut, Copenhagen, Denmark; 12)National Heart, Lung and Blood Institute's The Framingham Heart Study, Population Sciences Branch, Division of Intramural Research, Framingham MA 01702 USA; 13)deCODE Genetics, Amgen inc., Reykjavik, Iceland; 14)Department of Epidemiology, Harvard T.H. Chan School of Public Health, Boston, MA, USA; 15)Department of Nutrition, Harvard T.H. Chan School of Public Health, Boston, MA, USA; 16)Channing Laboratory, Department of Medicine, Brigham and Women's Hospital and Harvard Medical School, Boston, MA, USA; 17)Pharmacogenomics Centre, Biomedical Research Institute, University of Dundee, Ninewells Hospital, Dundee, UK; 18)Department of Biostatistics, Boston University School of Public Health, Boston, MA, USA; 19)Department of Biostatistics, Harvard School of Public Health, Boston, MA, USA; 20)Lund University Diabetes Centre, Department of Clincal Science Malmö, University Hospital Scania, Lund University, 20502 Malmö, Sweden; 21)University of Pennsylvania - Perelman School of Medicine, Department of Pharmacology, Philadelphia PA, 19104, USA; 22)University of Pennsylvania - Perelman School of Medicine, Department of Genetics, Philadelphia PA, 19104, USA; 23)Institute of Translational Medicine and Therapeutics, University of Pennsylvania - Perelman School of Medicine, Philadelphia PA 19104, USA; 24)Research Unit of Molecular Epidemiology, Helmholtz Zentrum München, German Research Centre for Environmental Health, Neuherberg, Germany; 25)Institute of Epidemiology II, Helmholtz Zentrum München, German Research Center for Environmental Health, Neuherberg, Germany; 26)German Center for Diabetes Research, Neuherberg, Germany; 27)Institute of Genetic Epidemiology, Helmholtz Zentrum München, German Research Center for Environmental Health, Neuherberg, Germany; 28)Department of Medicine I, University Hospital Grosshadern, Ludwig-Maximilians-Universität, Munich, Germany; 29)Institute of Medical Informatics, Biometry and Epidemiology, Chair of Genetic Epidemiology, Ludwig-Maximilians-Universität, Munich, Germany; 30)DZHK (German Centre for Cardiovascular Research), partner site Munich Heart Alliance, Munich, Germany; 31)Oxford Centre for Diabetes, Endocrinology and Metabolism, University of Oxford, Oxford, UK; 32)Wellcome Trust Sanger Institute, Hinxton, UK; 33)Department of Epidemiology, Erasmus University Medical Center, Rotterdam, The Netherlands; 34)PolyOmica, Groningen, The Netherlands; 35)MRC Epidemiology Unit, University of Cambridge School of Clinical Medicine, Institute of Metabolic Science, Cambridge Biomedical Campus, Cambridge, UK; 36)High Throughput Biology Center, Johns Hopkins University School of Medicine, Baltimore, MD, USA; 37)Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA; 38)The Charles Bronfman Institute for Personalized Medicine, Icahn School of Medicine at Mount Sinai, New York, NY, USA; 39)The Genetics of Obesity and Related Metabolic Traits Program, The Icahn School of Medicine at Mount Sinai, New York,

NY, USA; 40)Inserm UMR1087,Institut du Thorax, Nantes, FRANCE; 41)CNRS UMR 6291, Nantes, FRANCE; 42)Centre Hospitalier Universitaire (CHU) Nantes, Nantes, FRANCE; 43)Université de Nantes, Nantes, FRANCE; 44)Lille Institute of Biology, European Genomics Institute of Diabetes, Lille, France; 45)CNRS-UMR-8199, Institute of Biology and Lille 2 University, Pasteur Institute, Lille, France; 46)Friedrich-Schiller University Jena and Leibniz Institute for Age Research, Fritz Lipmann Institute, Jena, Germany; 47)Research Group Bioinformatics and Systems Biology, Institute of Neural Information Processing, University of Ulm, Ulm, Germany; 48)Institute for Molecular Medicine Finland (FIMM), Helsinki, Finland; 49)Institute for Medical Informatics, Biometry and Epidemiology, University Hospital of Essen, Essen, Germany; 50)Department of Medical Sciences, Molecular Epidemiology and Science for Life Laboratory, Uppsala University, Uppsala, Sweden; 51)Atherosclerosis Research Unit, Department of Medicine Solna, Karolinska Institutet, Stockholm, Sweden; 52)Science for Life Laboratory, Stockholm, Sweden; 53)Department for Numerical Analysis and Computer Science, Stockholm University, Stockholm, Sweden; 54)Faculty of Medicine, University of Iceland, Reykjavik, Iceland; 55)Landspitali University Hospital, Reykjavik, Iceland; 56)Icelandic Heart Association, Kopavogur, Iceland; 57)Department of Biostatistics, Harvard T.H. Chan School of Public Health, Boston, MA, USA; 58)Institute of Human Genetics, Helmholtz Zentrum München, Neuherberg, Germany; 59)Department of Endocrinology and Diabetology, Medical Faculty, Heinrich-Heine University, Düsseldorf, Germany; 60)German Center for Diabetes Research (DZD e.V.), München-Neuherberg, Germany; 61)Institute for Clinical Diabetology, German Diabetes Center, Leibniz Institute for Diabetes Research at Heinrich Heine University Düsseldorf, Düsseldorf, Germany; 62)Division of Genetics and Endocrinology, Children's Hospital, Boston, MA, USA; 63)Program in Medical and Population Genetics, Broad Institute, Cambridge, MA, USA; 64)National Heart, Lung, and Blood Institute's Framingham Heart Study, Framingham, MA, USA; 65)Division of Endocrinology and Metabolism, Brigham and Women’s Hospital and Harvard Medical School, Boston, MA, USA; 66)Boston University Data Coordinating Center, Boston, MA, USA; 67)Folkhälsan Research Center, FIN-00014 Helsinki, Finland; 68)Dept of Social Services and Health Care, 68601 Jakobstad, Finland; 69)Department of Medicine, Helsinki University Hospital, University of Helsinki, 000290 HUS Helsinki , Finland; 70)Collaborative Studies Coordinating Center, Department of Biostatistics, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA; 71)Division of Epidemiology and Community Health, University of Minnesota, Minneapolis, MN, USA; 72)Steno Diabetes Center, Gentofte, Denmark; 73)Research Centre for Prevention and Health, Capital Region of Denmark, Copenhagen, Denmark; 74)Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark; 75)Faculty of Medicine, University of Aalborg, Aalborg, Denmark; 76)Copenhagen University Hospital, Rigshospitalet, Denmark.; 77)Department of Clinical Medicine, Faculty of Health and Medical Sciences, University of Copenhagen, Denmark; 78)Department of Preventive Medicine, Northwestern University Feinberg School of Medicine, Chicago, IL, USA; 79)Saw Swee Hock School of Public Health, National University of Singapore, Singapore, Singapore; 80)Channing Division of Network Medicine, Department of Medicine, Brigham and Women's Hospital and Harvard Medical School, Boston, MA, USA; 81)Program in Genetic Epidemiology and Statistical Genetics, Harvard T.H. Chan School of Public Health, Boston, MA, USA; 82)Oxford National Institute for Health Research Biomedical Research Centre, Churchill Hospital, Oxford, UK; 83)Genetics of Complex Traits, University of Exeter Medical School, University of Exeter, Exeter, UK; 84)National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, USA; 85)Department of Health, National Institute for Health and Welfare, Helsinki, Finland; 86)University of Helsinki and Helsinki University Central Hospital: Department of Medicine and Abdominal Center: Endocrinology, Helsinki,

Finland; 87)Minerva Foundation Institute for Medical Research, Biomedicum 2U, Helsinki, Finland; 88)Institute of Human Genetics, University of Bonn, Bonn, Germany; 89)Department of Genomics, Life & Brain Center, University of Bonn, Bonn, Germany; 90)Centro Cardiologico Monzino, Istituto di Ricovero e Cura a Carattere Scientifico (IRCCS), Milan, Italy; 91)Dipartimento di Scienze Farmacologiche e Biomolecolari, Università di Milano, Milan, Italy; 92)Cardiovascular Genetics, BHF Laboratories, Institute Cardiovascular Sciences, UCL, London, UK; 93)Research Unit of Molecular Epidemiology, Helmholtz Zentrum Muenchen, German Research Centre for Environmental Health, Neuherberg, Germany; 94)Hannover Unified Biobank, Hannover Medical School, Hannover, Germany; 95)Institute of Genetic Epidemiology, Helmholtz Zentrum Muenchen, German Research Center for Environmental Health, Neuherberg, Germany; 96)Department of Clinical Chemistry and Central Laboratory, University of Ulm, Ulm, Germany; 97)Department of Internal Medicine, Erasmus University Medical Center, Rotterdam, The Netherlands; 98)Department of Chronic Disease Prevention, National Institute for Health and Welfare, Helsinki, Finland; 99)Department of General Practice and Primary Health Care, University of Helsinki, Helsinki, Finland; 100)Unit of General Practice, Helsinki University Hospital, Helsinki, Finland; 101)Folkhalsan Research Center, Helsinki, Finland; 102)Broad Institute of Harvard and Massachusetts Institute of Technology, Cambridge, MA, USA; 103)Department of Public Health, Hjelt Institute, University of Helsinki, Helsinki, Finland; 104)Endocrinology-Diabetology Unit, Corbeil-Essonnes Hospital, Corbeil-Essonnes, France; 105)Division of Cardiovascular Epidemiology, Institute of Environmental Medicine, Karolinska Institutet, Stockholm, Sweden; 106)Division of Psychiatric Genomics, Department of Psychiatry, Icahn School of Medicine at Mount Sinai, New York, New York, USA; 107)IFB Adiposity Diseases, University of Leipzig, Leipzig, Germany; 108)Department of Medicine, University of Leipzig, Leipzig, Germany; 109)Department of Medicine, Division of General Internal Medicine, The Johns Hopkins Bloomberg School of Medicine, Baltimore, MD, USA; 110)The Welch Center for Prevention, Epidemiology, and Clinical Research, The Johns Hopkins University, Baltimore, MD, USA; 111)William Harvey Research Institute, Barts and The London School of Medicine and Dentistry, Queen Mary University London, London, UK; 112)Department of Statistics, University of Oxford, Oxford, UK; 113)Institute of Biomedical and Clinical Science, University of Exeter Medical School, Exeter, UK; 114)Public Health Genomics Unit, National Institute for Health and Welfare, Helsinki, Finland; 115)Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm, Sweden; 116)Division of Endocrinology and Diabetes, Department of Internal Medicine, University Medical Centre Ulm, Ulm, Germany; 117)Imperial College London, London, UK; 118)Lee Kong Chian School of Medicine, Nanyang Technological University, Singapore, Singapore; 119)Diabetes and Obesity Research Institute, Cedars-Sinai Medical Center, Los Angeles, CA, USA; 120)Department of Genetics, University of North Carolina, Chapel Hill, NC, USA; 121)Dasman Diabetes Institute, Dasman, Kuwait; 122)Centre for Vascular Prevention, Danube-University Krems, Krems, Austria; 123)Diabetes Research Group, King Abdulaziz University, Jeddah, Saudi Arabia; 124)Faculty of Health Sciences, University of Southern Denmark, Odense, Denmark; 125)University of Cambridge Metabolic Research Laboratories and NIHR Cambridge Biomedical Research Centre, Level 4, WT-MRC Institute of Metabolic Science Box 289 Addenbrooke's Hospital Cambridge, Cambridge, UK; 126)Department of Public Health and Caring Sciences, Uppsala University, Uppsala, Sweden; 127)Department of Medicine, Division of Cardiovascular Medicine, Stanford University School of Medicine, Stanford, USA; 128)Department of Medical Sciences, Uppsala University Hospital, Uppsala, Sweden; 129)Department of Genomics of Common Disease, Imperial College London, London, UK; 130)The Mindich Child Health and Development Institute, Icahn School of Medicine at Mount Sinai, New York, NY, USA; 131)Inserm, CESP, U1018, Villejuif, France; 132)Univ

Paris-Sud, UMRS 1018, Villejuif, France; 133)German Institute of Human Nutrition Potsdam-Rehbruecke, Germany; 134)Lund University, Malmö, Sweden; 135)Umeå University, Umeå, Sweden; 136)Navarra Public Health Institute, Pamplona, Spain; 137)Navarra Institute for Health Research (IdiSNA), Pamplona, Spain; 138)CIBER Epidemiology and Public Health (CIBERESP), Madrid, Spain; 139)Cancer Research and Prevention Institute (ISPO), Florence, Italy; 140)University Medical Center Utrecht, Utrecht, the Netherlands; 141)Broad Institute of Harvard and Massachusetts Institute of Technology (MIT), Cambridge, Massachusetts 02142, USA; 142)Center for Human Genetic Research, Massachusetts General Hospital, 185 Cambridge Street, Boston, Massachusetts 02114, USA; 143)Department of Medicine, Harvard Medical School, Boston, Massachusetts 02115, USA; 144)Department of Genetics, Harvard Medical School, Boston, Massachusetts 02115, USA; 145)Department of Molecular Biology, Harvard Medical School, Boston, Massachusetts 02115, USA; 146)Diabetes Unit, Massachusetts General Hospital, Boston, Massachusetts 02144, USA; 147)Institute for Molecular Medicine Finland (FIMM), University of Helsinki, Helsinki, Finland; 148)Netherlands Genomics Initiative, Netherlands Consortium for Healthy Ageing and Center for Medical Systems Biology, Rotterdam, The Netherlands; 149)Diabetes Unit and Center for Human Genetic Research, Massachusetts General Hospital, Boston, MA, USA; 150)Department of Medicine, Harvard Medical School, Boston, MA, USA; 151)General Medicine Division, Massachusetts General Hospital, MA, USA; 152)Human Genetics Center, University of Texas Health Science Center at Houston, Houston, TX, USA; 153)Human Genome Sequencing Center at Baylor College of Medicine, Houston, TX, USA; 154)Institute of Molecular and Cell Biology, University of Tartu, Tartu, Estonia; 155)Usher Institute of Population Health Sciences and Informatics, University of Edinburgh, Edinburgh, UK.; 156)Cardiovascular and Diabetes Medicine, Biomedical Research Institute, University of Dundee, Ninewells Hospital, Dundee, UK; 157)Department of Biostatistics, University of Liverpool, Liverpool, UK; 158)Department of Molecular and Clinical Pharmacology, University of Liverpool, Liverpool, UK; 159) Deceased.

* These authors contributed equally to this research.
# These authors jointly directed this research.

**Correspondence should be addressed to:**

**Dr. Inga Prokopenko**
Department of Genomics of Common Disease
School of Public Health, Imperial College London
Burlington Danes Building, Hammersmith Hospital,
Du Cane Road, London, W12 0NN, UK
Phone: +4420 759 46501
E-mail: i.prokopenko@imperial.ac.uk

**Prof. Mark I. McCarthy**
OCDEM, Churchill Hospital, University of Oxford
Old Road, Headington, OX3 7LJ, UK
Email: mark.mccarthy@drl.ox.ac.uk

**Prof. Michael Boehnke**
Department of Biostatistics and Center for Statistical Genetics
University of Michigan

School of Public Health
1415 Washington Heights
Ann Arbor, MI 48109-2029
Email: boehnke@umich.edu

**Abstract word count: 198**

**Main text word count: 4241**

**Figures: 3**

**Tables: 1**

**References: 51**

**ABSTRACT**

To characterise type 2 diabetes (T2D) associated variation across the allele frequency spectrum, we conducted a meta-analysis of genome-wide association data from 26,676 T2D cases and 132,532 controls of European ancestry after imputation using the 1000 Genomes multi-ethnic reference panel. Promising association signals were followed-up in additional data sets (of 14,545 or 7,397 T2D cases and 38,994 or 71,604 controls). We identified 13 novel T2D-associated loci ($p<5\times10^{-8}$), including variants near the *GLP2R*, *GIP*, and *HLA-DQA1* genes. Our analysis brought the total number of independent T2D associations to 128 distinct signals at 113 loci**.** Despite substantially increased sample size and more complete coverage of low-frequency variation, all novel associations were driven by common SNVs. Credible sets of potentially causal variants were generally larger than those based on imputation with earlier reference panels, consistent with resolution of causal signals to common risk haplotypes. Stratification of T2D-associated loci based on T2D-related quantitative trait associations revealed tissue-specific enrichment of regulatory annotations in pancreatic islet enhancers for loci influencing insulin secretion, and in adipocytes, monocytes and hepatocytes for insulin action-associated loci. These findings highlight the predominant role played by common variants of modest effect and the diversity of biological mechanisms influencing T2D pathophysiology.

**MAIN TEXT**

Type 2 diabetes (T2D) has rapidly increased in prevalence in recent years and represents a major component of the global disease burden (1). Previous efforts to use genome-wide association studies (GWAS) to characterise the genetic component of T2D risk have largely focused on common variants (minor allele frequency [MAF]>5%). These studies have identified close to 100 loci, almost all of them currently defined by common alleles associated with modest (typically 5-20%) increases in T2D risk (2–6). Direct sequencing of whole genomes or exomes offers the most comprehensive approach for extending discovery efforts to the detection of low-frequency (0.5%<MAF<5%) and rare (MAF<0.5%) risk and protective alleles, some of which might have greater impact on individual predisposition. However, extensive sequencing has, thus far, been limited to relatively small sample sizes (at most, a few thousand cases), restricting power to detect rarer risk alleles, even if they are of large effect (7–9). Whilst evidence of rare variant associations has been detected in some candidate gene studies (10,11), the largest study to date, involving exome sequencing in ~13,000 subjects, found little trace of rare variant association effects (9).

Here, we implement a complementary strategy that makes use of imputation into existing GWAS samples from the DIAbetes Genetics Replication And Meta-analysis (DIAGRAM) Consortium with sequence-based reference panels (12). This strategy allows the detection of common and low-frequency (but not rare) variant associations in extremely large samples (13), and facilitates the fine-mapping of causal variants. We performed a European ancestry meta-analysis of GWAS with 26,676 T2D cases and 132,532 controls, and followed up our findings in additional independent European ancestry studies of 14,545 T2D cases and 38,994 controls genotyped using the Metabochip (4). All contributing studies were imputed against the March 2012 multi-ethnic 1000 Genomes Project (1000G) reference panel of 1,092 whole-genome sequenced individuals (12). Our study provides near-complete evaluation of common

variants with much improved coverage of low-frequency variants, and the combined sample size considerably exceeds that of the largest previous T2D GWAS meta-analyses in individuals of European ancestry (4). In addition to genetic discovery, we fine-map novel and established T2D-associated loci to identify regulatory motifs and cell types enriched for potential causal variants, and pathways through which T2D-associated loci increase disease susceptibility.

## RESEARCH DESIGN AND METHODS

***Research participants.*** The DIAGRAM stage 1 meta-analyses is comprised of 26,676 T2D cases and 132,532 controls (effective sample size, $N_{eff}$=72,143 individuals, defined as $4/[(1/N_{cases})+(1/N_{controls})]$) from 18 studies genotyped using commercial genome-wide single-nucleotide variant (SNV) arrays (**Supplementary Table 1**). The Metabochip stage 2 follow up is comprised of 14,545 T2D cases and 38,994 controls ($N_{eff}$=38,645) from 16 non-overlapping stage 1 studies (4,14). We performed additional follow-up in 2,796 T2D cases and 4,601 controls from the EPIC-InterAct (15) and 9,747 T2D cases and 61,857 controls from the GERA study (16) (**Supplementary Material**).

***Statistical analyses.*** We imputed autosomal and X chromosome SNVs using the all ancestries 1000G reference panel (1,092 individuals from Africa, Asia, Europe, and the Americas [March, 2012 release]) using miniMAC (17) or IMPUTE2 (18). After imputation, from each study we removed monomorphic variants or those with imputation quality $r^2$-hat<0.3 (miniMAC) or proper-info<0.4 (IMPUTE2, SNPTEST). Each study performed T2D association analysis using logistic regression, adjusting for age, sex, and principal components for ancestry, under an additive genetic model. We performed inverse-variance weighted fixed-effect meta-analyses of the 18 stage 1 GWAS (**Supplementary Table 1**). Fifteen of the 18 studies repeated analyses also adjusting for body mass index (BMI). SNVs reaching suggestive significance $p<10^{-5}$ in the stage 1 meta-analysis were followed-up. Novel

loci were selected using the threshold for genome-wide significance ($p<5\times10^{-8}$) in the combined stage 1 and stage 2 meta-analysis. For the 23 variants with no proxy ($r^2\geq0.6$) available in Metabochip with 1000G imputation in the fine-mapping regions, the stage 1 result was followed-up in EPIC-InterAct and GERA, both imputed to 1000G variant density (**Supplementary Material**).

***Approximate conditional analysis with GCTA.*** We performed approximate conditional analysis in the stage 1 sample using GCTA v1.24 (19,20). We analysed SNVs in the 1Mb-window around each lead variant, conditioning on the lead SNV at each locus (**Supplementary Material**) (21). We considered loci to contain multiple distinct signals if multiple SNVs reached locus-wide significance ($p<10^{-5}$), accounting for the approximate number of variants in each 1Mb window (14).

***Fine-mapping analyses using credible set mapping.*** To identify 99% credible sets of causal variants for each distinct association signal, we performed fine-mapping for loci at which the lead independent SNV reached $p<5\times10^{-4}$ in the stage 1 meta-analysis. We performed credible set mapping using the T2D stage 1 meta-analysis results to obtain the minimal set of SNVs with cumulative posterior probability>0.99 (**Supplementary Material**).

***Type 1 diabetes (T1D)/T2D discrimination analysis.*** Given the overlap between loci previously associated with T1D and the associated T2D loci, we used an inverse variance weighted Mendelian randomisation approach (22) to test whether this was likely to reflect misclassification of T1D cases as individuals with T2D in the current study (**Supplementary Material**).

***Expression quantitative trait locus (eQTL) analysis.*** To look for potential biological overlap of T2D lead variants and eQTL variants, we extracted the lead (most significantly associated) eQTL for each tested gene from existing datasets for a range of tissues (**Supplementary**

**Material**). We concluded that a lead T2D SNV showed evidence of association with gene expression if it was in high LD ($r^2$>0.8) with the lead eQTL SNV ($p<5\times10^{-6}$).

***Hierarchical clustering of T2D-related metabolic phenotypes.*** Starting with the T2D associated SNVs, we obtained T2D-related quantitative trait Z-scores from published HapMap-based GWAS meta-analysis for: fasting glucose, fasting insulin adjusted for BMI, homeostasis model assessment for beta-cell function (HOMA-B), homeostasis model assessment for insulin resistance (HOMA-IR) (23); 2-hour glucose adjusted for BMI (24); proinsulin (25); corrected insulin response (CIR) (26); BMI (27); high density lipoprotein cholesterol (HDL-C), low density lipoprotein cholesterol (LDL-C), total cholesterol, and triglycerides (28). When an association result for a SNV was not available, we used the results for the variant in highest LD and only for variants with $r^2$>0.6. We performed clustering of phenotypic effects using Z-scores for association with T2D risk alleles and standard methods (**Supplementary Material**) (29).

***Functional annotation and enrichment analysis***. We tested for enrichment of genomic and epigenomic annotations using chromatin states for 93 cell types (after excluding cancer cell lines) from the NIH Epigenome Roadmap project, and binding sites for 165 transcription factors (TF) from ENCODE (30) and Pasquali et al. (31). Using fractional logistic regression, we then tested for the effect of variants with each cell type and TF annotation on the variant posterior probabilities ($\pi_c$) using all variants within 1Mb of the lead SNV for each distinct association signal from the fine-mapping analyses (**Supplementary Material**). In each analysis, we considered an annotation significant if it reached a Bonferroni-corrected $p<1.9\times10^{-4}$ (i.e. 0.05/258 annotations).

***Pathway analyses with DEPICT.*** We used the Data-driven Expression Prioritized Integration for Complex Traits (DEPICT) tool (32) to (i) prioritize genes that may represent promising candidates for T2D pathophysiology, and (ii) identify reconstituted gene sets that are

enriched in genes from associated regions and might be related to T2D biological pathways. As input, we used independent SNVs from the stage 1 meta-analysis SNVs with $p<10^{-5}$ and lead variants at established loci (**Supplementary Material**). For the calculation of empirical enrichment *p* values, we used 200 sets of SNVs randomly drawn from entire genome within regions matching by gene density; we performed 20 replications for false discovery rate (FDR) estimation.

**RESULTS**

***Novel loci detected in T2D GWAS and Metabochip-based follow-up.*** The stage 1 GWAS meta-analysis included 26,676 T2D cases and 132,532 controls and evaluated 12.1M SNVs, of which 11.8M were autosomal and 260k mapped to the X chromosome. Of these, 3.9M variants had MAF between 0.5% and 5%, a near fifteen-fold increase in the number of low-frequency variants tested for association compared to previous array-based T2D GWAS meta-analyses (2,4) (**Supplementary Table 2**). Of the 52 signals showing promising evidence of association ($p<10^{-5}$) in stage 1, 29 could be followed up in the stage 2 Metabochip data. In combined stage 1 and stage 2 data, 13 novel loci were detected at genome-wide significance (**Table 1, Figure 1, Supplementary Figure 1A-D, Supplementary Table 3**).

Lead SNVs at all 13 novel loci were common. Although detected here using 1000G imputed data, all 13 were well captured by variants in the HapMap CEU reference panel (2 directly, 10 via proxies with $r^2>0.8$, and one via proxy with $r^2=0.62$) (**Supplementary Materials**). At all 13, lead variants defined through 1000G and those seen when the SNP density was restricted to HapMap content, had broadly similar evidence of association and were of similar frequency (**Supplementary Figure 2; Supplementary Table 3**). Throughout this manuscript, loci are named for the gene nearest to the lead SNV, unless otherwise specified (**Table 1, Supplementary Materials: Biology box**).

Adjustment for BMI revealed no additional genome-wide significant associations for T2D and, at most known and novel loci, there were only minimal differences in statistical significance and estimated T2D effect size between BMI-adjusted and unadjusted models. The four signals at which we observed a significant effect of BMI adjustment ($p_{heterogeneity}<4.4\times10^{-4}$; based on 0.05/113 variants currently or previously reported to be associated with T2D at genome-wide significance) were *FTO* and *MC4R* (at which the T2D association is known to reflect a primary effect on BMI), and *TCF7L2* and *SLC30A8* (at which T2D associations were strengthened after BMI-adjustment) (**Supplementary Figure 3; Supplementary Table 4**).

***Insights into genetic architecture of T2D.*** In this meta-analysis, we tested 3.9M low-frequency variants ($r^2\geq0.3$ or proper-info$\geq$0.4; minor allele present in $\geq$3 studies) for T2D association, constituting 96.7% of the low-frequency variants ascertained by the 1000G European Panel (March 2012) (**Supplementary Table 2**). For variants with risk-allele frequencies (RAF) of 0.5%, 1%, or 5%, we had 80% power to detect association ($p<5\times10^{-8}$) for allelic ORs of 1.80, 1.48, and 1.16, respectively, after accounting for imputation quality (**Figure 1, Supplementary Table 5**). Despite the increased coverage and sample size, we identified no novel low-frequency variants at genome-wide significance (**Figure 1**). Since we had only been able to test 29 of the 52 promising stage 1 signals on the Metabochip, we investigated whether this failure to detect low-frequency variant associations with T2D could be a consequence of selective variant inclusion on the Metabochip. Amongst the remaining 23 variants, none reached genome-wide significance after aggregating with GWAS data available from EPIC-InterAct. Six of these 23 SNVs had MAF<5%, and for these we performed additional follow-up in the GERA study. However, none reached genome-wide significance in a combined analysis of stage 1, EPIC-InterAct and GERA (a total of 39,219 cases and 198,990 controls) (**Supplementary Table 6**). Therefore, despite substantially

enlarged sample sizes that would have allowed us to detect low-frequency risk alleles with modest effect sizes, the overwhelming majority of variants for which T2D-association can be detected with these sample sizes are themselves common.

To identify loci containing multiple distinct signals, we performed approximate conditional analysis within the established and novel GWAS loci and detected two such novel common variant signals (**Supplementary Table 7**) (19,20). At the *ANKRD55* locus, we identified a previously-unreported distinct ($p_{conditional}<10^{-5}$) association signal led by rs173964 ($p_{conditional}=3.54\times10^{-7}$, MAF=26%) (**Supplementary Table 7, Supplementary Figure 4**). We also observed multiple signals of association at loci with previous reports of such signals (4,14), including *CDKN2A/B* (3 signals in total), *DGKB*, *KCNQ1* (6 signals), *HNF4A*, and *CCND2* (3 signals) (**Supplementary Table 7, Supplementary Figure 4**). At *CCND2,* in addition to the main signal with lead SNV rs4238013, we detected: (i) a novel distinct signal led by a common variant, rs11063018 ($p_{conditional}=2.70\times10^{-7}$, MAF=19%); and (ii) a third distinct signal led by a low-frequency protective allele (rs188827514, MAF=0.6%; $OR_{conditional}=0.60$, $p_{conditional}=1.24\times10^{-6}$) (**Supplementary Figure 5A, Supplementary Table 7**), which represents the same distinct signal as that at rs76895963 ($p_{conditional}=1.0$) reported in the Icelandic population (**Supplementary Figure 5B**) (7). At *HNF4A,* we confirm recent analyses (obtained in partially-overlapping data) (14) that a low-frequency missense variant (rs1800961, p.Thr139Ile, MAF=3.7%) is associated with T2D, and is distinct from the known common variant GWAS signal (which we map here to rs12625671).

We evaluated the trans-ethnic heterogeneity of allelic effects (i.e. discordance in the direction and/or magnitude of estimated odds ratios) at novel loci on the basis of Cochran's Q statistics from the largest T2D trans-ancestry GWAS meta-analysis to date (2). Using reported summary statistics from that study, we observed no significant evidence of heterogeneity of effect size (Bonferroni correction $p_{Cochran's\ Q}<0.05/13=0.0038$) between major ancestral

groups at any of the 13 loci (**Supplementary Table 8**). These results are consistent with these loci being driven by common causal variants that are widely distributed across populations.

***1000G variant density for identification of potentially causal genetic variants.*** We used credible set fine-mapping (33) to investigate whether 1000G imputation allowed us to better resolve the specific variants driving 95 distinct T2D association signals at 82 loci (**Supplementary Material**). 99% credible sets included between 1 and 7,636 SNVs; 25 included fewer than 20 SNVs, 16 fewer than 10 (**Supplementary Tables 9 and 10**). We compared 1000G-based credible sets with those constructed from HapMap SNVs alone (**Figure 2B**, **Supplementary Table 9**). At all but three of the association signals (two at *KCNQ1* and rs1800961 at *HNF4A*), 1000G imputation resulted in larger credible sets (median increase of 34 variants) spanning wider genomic intervals (median interval size increase of 5kb) (**Figure 2B, Supplementary Table 9**). The 1000G-defined credible sets included >85% of the SNVs in the corresponding HapMap sets (**Supplementary Table 9**). Despite the overall larger credible sets, we asked whether 1000G imputation enabled an increase in the posterior probability afforded to the lead SNVs, but found no evidence to this effect (**Figure 2C**).

Within the 50 loci previously associated with T2D in Europeans (4) which had at least modest evidence of association in the current analyses ($p<5x10^{-4}$), we asked whether the lead SNV in 1000G-imputed analysis was of similar frequency to that observed in HapMap analyses. Only at *TP53INP1*, was the most strongly associated 1000G-imputed SNV (rs11786613, OR=1.21, $p=1.6x10^{-6}$, MAF=3.2%) of substantially lower frequency than the lead HapMap-imputed SNV (3) (rs7845219, MAF=47.7%, **Figure 2A**). rs11786613 was neither present in HapMap, nor on the Metabochip (**Supplementary Figure 6**). Reciprocal conditioning of this low-frequency SNV and the previously identified common lead SNV

(rs7845219: OR=1.05, p=5.0x$10^{-5}$, MAF=47.5%) indicated that the two signals were likely to be distinct but the signal at rs11786613 did not meet our threshold ($p_{conditional}<10^{-5}$) for locus-wide significance (**Supplementary Figure 4**).

***Pathophysiological insights from novel T2D associations.*** Among the 13 novel T2D-associated loci, many (such as those near *HLA-DQA1*, *NRXN3*, *GIP*, *ABO* and *CMIP*) included variants previously implicated in predisposition to other diseases and traits ($r^2>0.6$ with the lead SNV) (**Supplementary Table 3, Supplementary Materials: Biology box**). For example, the novel association at SNV rs1182436 lies ~120Kb upstream of *MNX1*, a gene implicated in pancreatic hypoplasia and neonatal diabetes (34–36).

The lead SNV rs78761021 at the *GLP2R* locus, encoding the receptor for glucagon-like peptide 2, is in strong LD ($r^2=0.87$) with a common missense variant in *GLP2R* (rs17681684, D470N, p=3×$10^{-7}$). These signals were strongly dependent and mutually extinguished in reciprocal conditional analyses, consistent with the coding variant being causal and implicating *GLP2R* as the putative causal gene (**Supplementary Figure 7**). While previously suggested to regulate energy balance and glucose tolerance (37), GLP2R has primarily been implicated in gastrointestinal function (38,39). In contrast, *GLP1R*, encoding the GLP-1 receptor (the target for a major class of T2D therapies (40)) is more directly implicated in pancreatic islet function and variation at this gene has been associated with glucose levels and T2D risk (41).

We also observed associations with T2D centred on rs9271774 near *HLA-DQA1* (**Table 1**), a region showing a particularly strong association with T1D (42). There is considerable heterogeneity within, and overlap between, the clinical presentations of T1D and T2D, but these can be partially resolved through measurement of islet cell autoantibodies (43). Such measures were not uniformly available across studies contributing to our meta-analysis (**Supplementary Table 1**). We therefore considered whether the adjacency between T1D-

and T2D-risk loci was likely to reflect misclassification of individuals with autoimmune diabetes as cases in the present study.

Three lines of evidence make this unlikely. First, the lead T1D-associated SNV in the HLA region (rs6916742) was only weakly associated with T2D in the present study (p=0.01), and conditioning on this variant had only modest impact on the T2D-association signal at rs9271774 ($p_{unconditional}=3.3x10^{-7}$; $p_{conditional}=9.1x10^{-6}$). Second, of 52 published genome-wide significant T1D-association GWAS signals, 50 were included in the current analysis: only six of these reached even nominal association with T2D (p<0.05; **Supplementary Figure 8**), and at one of these six (*BCAR1*), the T1D risk-allele was *protective* for T2D. Third, in genetic risk score (GRS) analyses, the combined effect of these 50 T1D signals on T2D risk was of only nominal significance (OR =1.02[1.00, 1.03], p=0.026), and significance was eliminated when the 6 overlapping loci were excluded (OR =1.00[0.98, 1.02], p=0.73). In combination, these findings argue against substantial misclassification and indicate that the signal at *HLA-DQA1* is likely to be a genuine T2D signal.

***Potential genes and pathways underlying the T2D loci: eQTL and pathway analysis.*** Cis-eQTLs analyses highlighted four genes as possible effector transcripts: *ABO* (pancreatic islets), *PLEKHA1* (whole blood), *HSD17B12* (adipose, liver, muscle, whole blood) at the respective loci, and *HLA-DRB5* expression (adipose, pancreatic islets, whole blood) at the *HLA-DQA1* locus (**Supplementary Table 11**).

We next asked whether large-scale gene expression data, mouse phenotypes, and protein-protein interaction (PPI) networks could implicate specific gene candidates and gene sets in the aetiology of T2D. Using DEPICT (32), 29 genes were prioritised as driving observed associations (FDR<0.05), including *ACSL1* and *CMIP* among the genes mapping to the novel loci (**Supplementary Table 12**). These analyses also identified 20 enriched reconstituted gene sets (FDR<5%) falling into 4 groups (**Supplementary Figure 9;** complete results,

including gene prioritisation, can be downloaded from https://onedrive.live.com/redir?resid=7848F2AF5103AA1B!1505&authkey=!AIC31supgUwjZVU&ithint=file%2cxlsx). These included pathways related to mammalian target of rapamycin (mTOR), based on co-regulation of the *IDE*, *TLE1*, *SPRY2*, *CMIP*, and *MTMR3* genes (44).

***Overlap of associated variants with regulatory annotations.*** We observed significant enrichment for T2D-associated credible set variants in pancreatic islet active enhancers and/or promoters (log odds [β]=0.74, $p=4.2x10^{-8}$) and FOXA2 binding sites (β=1.40, $p=4.1\times10^{-7}$), as previously reported (**Supplementary Table 13**) (14). We also observed enrichment for T2D-associated variants in coding exons (β=1.56, $p=7.9x10^{-5}$), in EZH2-binding sites across many tissues (β=1.35, $p=5.3x10^{-6}$), and in binding sites for NKX2.2 (β=1.73, $p=4.1x10^{-8}$) and PDX1 (β=1.46, $p=7.4x10^{-6}$) in pancreatic islets (**Supplementary Figure 10**).

Even though credible sets were generally larger, analyses performed on the 1000G imputed results produced stronger evidence of enrichment than equivalent analyses restricted to SNVs present in HapMap. This was most notably the case for variants within coding exons (β=1.56, $p=7.9x10^{-5}$ in 1000G compared to β=0.68, p=0.62 in HapMap), and likely reflects more complete capture of the true causal variants in the more densely imputed credible sets. Single lead SNVs overlapping an enriched annotation accounted for the majority of the total posterior probability ($\pi_c>0.5$) at seven loci. For example, the lead SNV (rs8056814) at *BCAR1* ($\pi_c=0.57$) overlaps an islet enhancer (**Supplementary Figure 11A**), while the newly-identified low-frequency signal at *TP53INP1* overlaps an islet promoter element (rs117866713; $\pi_c=0.53$) (**Figure 2D**) (31).

We applied hierarchical clustering to the results of diabetes-related quantitative trait associations for the set of T2D-associated loci from the present study, identifying three main

clusters of association signals with differing impact on quantitative traits (**Supplementary Table 9**). The first, including *GIPR, C2CDC4A, CDKAL1, GCK, TCF7L2, GLIS3, THADA, IGF2BP2,* and *DGKB* involved loci with a primary impact on insulin secretion and processing (26,29). The second cluster captured loci (including *PPARG*, *KLF14*, and *IRS1*) disrupting insulin action. The third cluster, showing marked associations with BMI and lipid levels, included *NRXN3, CMIP, APOE,* and *MC4R,* but not *FTO*, which clustered alone.

In regulatory enhancement analyses, we observed strong tissue-specific enrichment patterns broadly consistent with the phenotypic characteristics of the physiologically-stratified locus subsets. The cluster of loci disrupting insulin secretion showed the most marked enrichment for pancreatic islet regulatory elements ($\beta$=0.91, p=$9.5\times10^{-5}$). In contrast, the cluster of loci implicated in insulin action was enriched for annotations from adipocytes ($\beta$=1.3, p=$2.7\times10^{-11}$) and monocytes ($\beta$=1.4, p=$1.4\times10^{-12}$), and that characterised by associations with BMI and lipids showed preferential enrichment for hepatic annotations ($\beta$=1.15, p=$5.8\times10^{-4}$) (**Figure 3A-C**). For example, at the novel T2D-associated *CMIP* locus, previously associated with adiposity and lipid levels (28,45), the lead SNV (rs2925979, $\pi_c$=0.91) overlaps an active enhancer element in both liver and adipose tissue, among others (**Supplementary Figure 11B**).

## DISCUSSION

In this large-scale study of T2D genetics, in which individual variants were assayed in up to 238,209 subjects, we identify 13 novel T2D-associated loci at genome-wide significance and refine causal variant location for the 13 novel and 69 established T2D loci. We also provide evidence for enrichment in regulatory elements at associated loci in tissues relevant for T2D, and demonstrate tissue-specific enrichment in regulatory annotations when T2D loci were stratified according to inferred physiological mechanism.

Together with loci reported in other recent publications (9), we calculate that the present analysis brings the total number of independent T2D associations to 128 distinct signals at 113 loci (**Supplementary Table 3**). Lead SNVs at all 13 novel loci were common (MAF > 0.15) and of comparable effect size (1.07≤OR≤1.10) to previously-identified common variant associations (2,4). Associations at the novel loci showed homogeneous effects across diverse ethnicities, supporting the evidence for coincident common risk alleles across ancestry groups (2). Moreover, we conclude that misclassification of diabetes subtype is not a major concern for these analyses and that the *HLA-DQA1* signal represents genuine association with T2D, independent of nearby signals that influence T1D.

We observed a general increase in the size of credible sets with 1000G imputation compared to HapMap imputation. This is likely due to improved enumeration of potential causal common variants on known risk haplotypes, rather than resolution towards low-frequency variants of larger effect driving common variant associations. These findings are consistent with the inference (arising also from the other analyses reported here) that the T2D-risk signals identified by GWAS are overwhelmingly driven by common causal variants. In such a setting, imputation with denser reference panels, at least in ethnically restricted samples, provides more complete elaboration of the allelic content of common risk haplotypes. Finer resolution of those haplotypes that would provide greater confidence in the location of causal variants will likely require further expansion of trans-ethnic fine-mapping efforts (2). The distinct signals at the established *CCND2* and *TP53INP1* loci point to contributions of low-frequency variant associations of modest effect, but indicate that even larger samples will be required to robustly detect association signals at low frequency.

The discovery of novel genome-wide significant association signals in the current analysis is attributable primarily to increased sample size, rather than improved genomic coverage. Although we queried a large proportion of the low-frequency variants present in the 1000G

European reference haplotypes, and had >80% power to detect genome-wide significant associations with OR>1.8 for the tested low-frequency risk variants, we found no such low-frequency variant associations in either established or novel loci. Whilst low-frequency variant coverage in the present study was not complete, this observation adds to the growing evidence (2,4,9,46) that few low-frequency T2D-risk variants with moderate to strong effect sizes exist in European ancestry samples, and is consistent with a primary role for common variants of modest effect in T2D risk. The present study reinforces the conclusions from a recent study which imputed from whole-genome sequencing data - from 2,657 European T2D cases and controls, rather than 1000G - into a set of GWAS studies partially overlapping with the present meta-analysis. We demonstrated that the failure to detect low frequency associations in that study is not overcome by a substantial increase in sample size (9). It is worth emphasising that we did not, in this study, have sufficient imputation quality to test for T2D associations with rare variants and we cannot evaluate the collective contribution of variants with MAF<0.5% to T2D risk.

The development of T2D involves dysfunction of multiple mechanisms across several distinct tissues (9,29,31,47,48). When coupled with functional data, we saw larger effect estimates for enrichment of coding variants than observed with HapMap SNVs alone, consistent with more complete recovery of the causal variants through imputation using a denser reference panel. The functional annotation analyses also demonstrated that the stratification of T2D-risk loci according to primary physiological mechanism resulted in evidence for consistent and appropriate tissue-specific effects on transcriptional regulation. These analyses exemplify the use of a combination of human physiology and genomic annotation to position T2D GWAS loci with respect to the cardinal mechanistic components of T2D development. Extension of this approach is likely to provide a valuable *in silico* strategy to aid prioritisation of tissues for mechanistic characterisation of genetic

associations. Using the hypothesis-free pathway analysis of T2D associations with DEPICT (32), we highlighted a causal role of mTOR signalling pathway in the aetiology of T2D not observed from individual loci associations. The mTOR pathway has previously been implicated in the link between obesity, insulin resistance, and T2D from cell and animal models (44,49).

The current results emphasize that progressively larger sample sizes, coupled with higher density sequence-based imputation (13), will continue to represent a powerful strategy for genetic discovery in T2D, and in complex diseases and traits more generally. At known T2D-associated loci, identification of the most plausible T2D causal variants will likely require large-scale multi-ethnic analyses, where more diverse haplotypes, reflecting different patterns of LD, in combination with functional (31,50,51) data allow refinement of association signals to smaller numbers of variants (2).

## DESCRIPTION OF SUPPLEMENTAL DATA

Supplemental Data include eleven figures and thirteen tables.

## AUTHOR CONTRIBUTIONS:

**Writing and co-ordination group:**

R.A.S., L.J.S., R.M., L.M., K.J.G., M.K., J.D., A.P.M., M.B., M.I.M., I.P.

**Central analysis group:**

R.A.S., L.J.S., R.M., L.M., C.M., A.P.M., M.B., M.I.M., I.P.

**Additional lead analysts:**

L.M., K.J.G., M.K., N.P., T.H.P., A.D.J., J.D.E., T.F., Y.Lee, J.R.B.P., L.J., A.U.J.

**GWAS cohort-level primary analysts:**

R.A.S., L.J.S., R.M., K.J.G., V.S., G.T., L.Q., N.R.V., A.Mahajan, H.Chen, P.A., B.F.V., H.G., M.M., J.S.R., N.W.R., N.R., L.C.K., E.M.L., S.M.W., C.Fuchsberger, P.K., C.M., P.C., M.L., Y.L., C.D., D.T., L.Y., C.Langenberg, A.P.M., I.P.

**Metabochip cohort-level primary analysts:**

T.S., H.K., H.C., L.E., S.G., T.M.T, M.F., R.J.S.

**Cohort sample collection, phenotyping, genotyping or additional analysis:**

R.A.S., H.G., R.B., A.B.H., A.K., G.S., N.D.K., J.L., L.L., T.M., M.R., B.T., T.E., E.M., C.F., C.L., D.Rybin, B.I., V.L., T.T., D.J.C., J.S.P., N.G., C.T.H., M.E.J., T.J., A.L., M.C.C., R.M.D., D.J.H., P.Kraft, Q.S., S.E., K.R.O., J.R.B.P., A.R.W., E.Z., J.T.-F., G.R .A., L.L.B., P.S.C., H.M.S., H.A.K., L.K., B.S., T.W.M., M.M.N., S.P., D.B., K.G., S.E.H., E.Tremoli, N.K., J.M., G.Steinbach, R.W., J.G .E., S.M., L.P., E.T., G.C., E.E., S.L., B.G., K.L., O.M., E.P.B., O.G., D.R., M.Blüher, P.Kovacs, A.T., N.M.M., C.S., T.M.F., A.T.H., I.B., B.B., H.B., P.W.F., A.B.G., D.P., Y.T.v.d.S., C.Langenberg, N.J.W., K.Strauch, M.B., M.I.M.

**Metabochip cohort principal investigators:**

R.E., K.J., S.Moebus, U.d.F., A.H., M.S., P.D., P.J.D., T.M.F., A.T.H., S.R., V.Salomaa, N.L.P., B.O.B., R.N.B., F.S.C., K.L.M., J.T., T.H., O.B.P., I.B., C.Langenberg, N.J.W.

**GWAS cohort principal investigators:**

L.Lannfelt, E.I., L.Lind, C.M.L., S.C., P.F., R.J.F.L., B.B., H.B., P.W.F., A.B.G., D.P., Y.T.v.d.S., D.A., L.C.G., C.Langenberg, N.J.W., E.S., C.Duijn van, J.C.F., J.B.M., E.B., C.G., K.Strauch, A.M., A.D.M., C.N.A.P., F.B.H., U.T., K.S., J.D., M.B., M.I.M.

## References


1. Global Burden of Disease Study 2013 Collaborators. Global, regional, and national incidence, prevalence, and years lived with disability for 301 acute and chronic diseases and injuries in 188 countries, 1990-2013: a systematic analysis for the Global Burden of Disease Study 2013. 2015;386:743–800.
2. DIAbetes Genetics Replication And Meta-analysis (DIAGRAM) Consortium, Asian Genetic Epidemiology Network Type 2 Diabetes (AGEN-T2D) Consortium, South Asian Type 2 Diabetes (SAT2D) Consortium, Mexican American Type 2 Diabetes (MAT2D) Consortium, Type 2 Diabetes Genetic Exploration by Nex-generation sequencing in muylti-Ethnic Samples (T2D-GENES) Consortium, Mahajan A, et al. Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nat Genet. 2014;46:234–44.
3. Voight BF, Scott LJ, Steinthorsdottir V, Morris ADP, Dina C, Welch RP, et al. Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nat Genet. 2010;42:579–89.
4. Morris AP, Voight BF, Teslovich TM, Ferreira T, Segrè AV, Steinthorsdottir V, et al. Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nat Genet. 2012;44:981–90.
5. Zeggini E, Scott LJ, Saxena R, Voight BF, Marchini JL, Hu T, et al. Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nat Genet. 2008;40:638–45.
6. Dupuis J, Langenberg C, Prokopenko I, Saxena R, Soranzo N, Jackson AU, et al. New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nat Genet. 2010;42:105–16.
7. Steinthorsdottir V, Thorleifsson G, Sulem P, Helgason H, Grarup N, Sigurdsson A, et al. Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. Nat Genet.2014;46:294–8.
8. Estrada K, Aukrust I, Bjørkhaug L, Burtt NP, Mercader JM, García-Ortiz H, et al. Association of a low-frequency variant in HNF1A with type 2 diabetes in a Latino population. JAMA. 2014;311:2305–14.
9. Fuchsberger C, Flannick J, Teslovich TM, Mahajan A, Agarwala V, Gaulton KJ, et al. The genetic architecture of type 2 diabetes. Nature. 2016;536:41-7.
10. Majithia AR, Flannick J, Shahinian P, Guo M, Bray M-A, Fontanillas P, et al. Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. Proc Natl Acad Sci U S A. 2014;111:13127-32.
11. Bonnefond A, Clement N, Fawcett K, Yengo L, Vaillant E, Guillaume J-L, et al. Rare MTNR1B variants impairing melatonin receptor 1B function contribute to type 2 diabetes. Nat Genet. 2012;44:297–301.
12. Abecasis GR, Auton A, Brooks LD, DePristo M a, Durbin RM, Handsaker RE, et al. An integrated map of genetic variation from 1,092 human genomes. Nature. 2012;491:56–65.
13. Yang J, Bakshi A, Zhu Z, Hemani G, Vinkhuyzen AAE, Lee SH, et al. Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. Nat Genet. 2015;47:1114–20.
14. Gaulton KJ, Ferreira T, Lee Y, Raimondo A, Mägi R, Reschen ME, et al. Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nat Genet. 2015;47:1415–25.
15. Langenberg C, Sharp S, Forouhi NG, Franks PW, Schulze MB, Kerrison N, et al. Design and cohort description of the InterAct Project: an examination of the

interaction of genetic and lifestyle factors on the incidence of type 2 diabetes in the EPIC Study. Diabetologia. 2011;54:2272–82.
16. Cook JP, Morris AP. Multi-ethnic genome-wide association study identifies novel locus for type 2 diabetes susceptibility. Eur J Hum Genet. 2016;24:1175–80.
17. Howie B, Fuchsberger C, Stephens M, Marchini J, Abecasis GR. Fast and accurate genotype imputation in genome-wide association studies through pre-phasing. Nat Genet. 2012;44:955–9.
18. Howie BN, Donnelly P, Marchini J. A flexible and accurate genotype imputation method for the next generation of genome-wide association studies. PLoS Genet. 2009;5:e1000529.
19. Yang J, Ferreira T, Morris AP, Medland SE, Madden PAF, Heath AC, et al. Conditional and joint multiple-SNP analysis of GWAS summary statistics identifies additional variants influencing complex traits. Nat Genet. 2012;44:369–75.
20. Yang J, Lee SH, Goddard ME, Visscher PM. GCTA: a tool for genome-wide complex trait analysis. Am J Hum Genet. 2011;88:76–82.
21. UK10K Consortium, Writing group, Production group, Cohorts group, Neurodevelopmental disorders group, Obesity group, et al. The UK10K project identifies rare variants in health and disease. Nature. 2015;526:82–90.
22. Burgess S, Butterworth A, Thompson SG. Mendelian randomization analysis with multiple genetic variants using summarized data. Genet Epidemiol. 2013;37:658–65.
23. Manning AK, Hivert M-F, Scott RA, Grimsby JL, Bouatia-Naji N, Chen H, et al. A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nat Genet. 2012;44:659–69.
24. Saxena R, Hivert M-F, Langenberg C, Tanaka T, Pankow JS, Vollenweider P, et al. Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nat Genet. 2010;42:142–8.
25. Strawbridge RJ, Dupuis J, Prokopenko I, Barker A, Ahlqvist E, Rybin D, et al. Genome-wide association identifies nine common variants associated with fasting proinsulin levels and provides new insights into the pathophysiology of type 2 diabetes. Diabetes. 2011;60:2624–34.
26. Prokopenko I, Poon W, Mägi R, Prasad B R, Salehi SA, Almgren P, et al. A central role for GRB10 in regulation of islet function in man. PLoS Genet. 2014;10:e1004235.
27. Speliotes EK, Willer CJ, Berndt SI, Monda KL, Thorleifsson G, Jackson AU, et al. Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nat Genet. 2010;42:937–48.
28. Willer CJ, Schmidt EM, Sengupta S, Peloso GM, Gustafsson S, Kanoni S, et al. Discovery and refinement of loci associated with lipid levels. Nat Genet. 2013;45:1274–83.
29. Dimas AS, Lagou V, Barker A, Knowles JW, Mägi R, Hivert MF, et al. Impact of type 2 diabetes susceptibility variants on quantitative glycemic traits reveals mechanistic heterogeneity. Diabetes. 2014;63:2158–71.
30. Dunham I, Kundaje A, Aldred SF, Collins PJ, Davis CA, Doyle F, et al. An integrated encyclopedia of DNA elements in the human genome. Nature. 2012;489:57–74.
31. Pasquali L, Gaulton KJ, Rodríguez-Seguí S a, Mularoni L, Miguel-Escalada I, Akerman I, et al. Pancreatic islet enhancer clusters enriched in type 2 diabetes risk-associated variants. Nat Genet. 2014;46:136–43.
32. Pers TH, Karjalainen JM, Chan Y, Westra H, Wood AR, Yang J, et al. Biological interpretation of genome-wide association studies using predicted gene functions. Nat Commun. 2015;6:5890.
33. Maller JB, McVean G, Byrnes J, Vukcevic D, Palin K, Su Z, et al. Bayesian refinement of association signals for 14 loci in 3 common diseases. Nat Genet.

2012;44:1294–301.
34. Flanagan SE, De Franco E, Lango Allen H, Zerah M, Abdul-Rasoul MM, Edge JA, et al. Analysis of transcription factors key for mouse pancreatic development establishes NKX2-2 and MNX1 mutations as causes of neonatal diabetes in man. Cell Metab. 2014;19:146–54.
35. Mele M, Ferreira PG, Reverter F, DeLuca DS, Monlong J, Sammeth M, et al. The human transcriptome across tissues and individuals. Science. 2015;348:660–5.
36. Bonnefond A, Vaillant E, Philippe J, Skrobek B, Lobbens S, Yengo L, et al. Transcription factor gene MNX1 is a novel cause of permanent neonatal diabetes in a consanguineous family. Diabetes Metab. 2013;39:276–80.
37. Guan X. The CNS glucagon-like peptide-2 receptor in the control of energy balance and glucose homeostasis. Am J Physiol Regul Integr Comp Physiol. 2014;307:R585-96.
38. Murphy KG, Bloom SR. Gut hormones and the regulation of energy homeostasis. Nature. 2006;444:854–9.
39. GTEx Consortium. Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans. Science. 2015;348:648–60.
40. Drucker DJ, Nauck MA. The incretin system: glucagon-like peptide-1 receptor agonists and dipeptidyl peptidase-4 inhibitors in type 2 diabetes. Lancet. 2006;368:1696–705.
41. Wessel J, Chu AY, Willems SM, Wang S, Yaghootkar H, Brody JA, et al. Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nat Commun. 2015;6:5897.
42. Bradfield JP, Qu H-Q, Wang K, Zhang H, Sleiman PM, Kim CE, et al. A genome-wide meta-analysis of six type 1 diabetes cohorts identifies multiple associated loci. PLoS Genet. 2011;7:e1002293.
43. NICE guideline. Type 1 diabetes in adults: diagnosis and management [article online]. 2015. Available from: nice.org.uk/guidance/ng17. Accessed 16 March 2017.
44. Zoncu R, Efeyan A, Sabatini DM. mTOR: from growth signal integration to cancer, diabetes and ageing. Nat Rev Mol Cell Biol. 2011;12(1):21–35.
45. Shungin D, Winkler TW, Croteau-Chonka DC, Ferreira T, Locke AE, Mägi R, et al. New genetic loci link adipose and insulin biology to body fat distribution. Nature. 2015;518:187–96.
46. Agarwala V, Flannick J, Sunyaev S, Altshuler D. Evaluating empirical bounds on complex disease genetic architecture. Nat Genet. 2013;45:1418–27.
47. Stumvoll M, Goldstein BJ, Van Haeften TW. Type 2 diabetes: Principles of pathogenesis and therapy. Lancet. 2005;365:1333–46.
48. Parker SCJ, Stitzel ML, Taylor DL, Orozco JM, Erdos MR, Akiyama JA, et al. Chromatin stretch enhancer states drive cell-specific gene regulation and harbor human disease risk variants. Proc Natl Acad Sci U S A. 2013;110:17921–6.
49. Dann SG, Selvaraj A, Thomas G. mTOR Complex1–S6K1 signaling: at the crossroads of obesity, diabetes and cancer. Trends Mol Med. 2007;13:252–9.
50. Claussnitzer M, Dankel SN, Klocke B, Grallert H, Glunk V, Berulava T, et al. Leveraging cross-species transcription factor binding site patterns: from diabetes risk Loci to disease mechanisms. Cell. 2014;156:343–58.
51. Farh KK, Marson A, Zhu J, Kleinewietfeld M, Housley WJ, Beik S, et al. Genetic and epigenetic fine mapping of causal autoimmune disease variants. Nature. 2014;518:337–43.

## FIGURE TITLES AND LEGENDS

**Figure 1.** The effect sizes of the established (blue diamonds, N=69, $p<5\times10^{-4}$, **Supplementary Material**), novel (red diamonds, N=13), and additional distinct (sky blue diamonds, N=13, **Supplementary Table 7**) signals according to their risk allele frequency (**Supplementary Table 3**). The additional distinct signals are based on approximate conditional analyses. The distinct signal at *TP53INP1* led by rs11786613 (**Supplementary Table 7**) is plotted (sky blue diamond). This signal did not reach locus-wide significance, but was selected for follow-up because of its low frequency and absence of LD with previously reported signal at this locus. The power curve shows the estimated effect size for which we had 80% power to detect associations. Established common variants with OR>1.12 are annotated.

**Figure 2**. A) The number of SNVs included in 99% credible sets when performed on all SNVs compared to when analyses were restricted to those SNVs present in HapMap. B) The cumulative $\pi_c$ of the top 3 SNVs among all 1000G SNVs and after restriction to HapMap SNVs is shown. While the low frequency SNV at *TP53INP1* (rs11786613) did not reach the threshold for a distinct signal in approximate conditional analyses, we fine-mapped both this variant and the previous common signal separately after reciprocal conditioning, which suggested they were independent. C) The minor allele frequency of the lead SNV identified in current analyses compared to that identified among SNVs present in HapMap. D) The association of the low frequency variant rs11786613 (blue) and that of the previous lead variant at this locus, rs7845219 (purple). The low frequency variant overlaps regulatory annotations active in pancreatic islets, among other tissues, and the sequence surrounding the A allele of this variant has a *in silico* recognition motif for a FOXA1:AR (androgen receptor) protein complex.

**Figure 3**. Type 2 diabetes loci stratified by patterns of quantitative trait (e.g. glycaemic, insulin, lipid, and anthropometric) effects show distinct cell-type annotation patterns. We hierarchically clustered loci based on endophenotype data and identified groups of T2D loci associated with measures of A) insulin secretion, B) insulin resistance, and C) BMI/lipids. We then tested the effect of variants in cell-type enhancer and promoter chromatin states on the posterior probabilities of credible sets for each group. We identified most significant effects among pancreatic islet chromatin for insulin secretion loci, CD14+ monocyte and adipose chromatin for insulin resistance loci, and liver chromatin for BMI/lipid loci.

**COMPETING FINANCIAL INTERESTS STATEMENT**

Inês Barroso and spouse own stock in GlaxoSmithKline and Incyte.

Jose C Florez has received consulting honoraria from Pfizer and PanGenX.

Valgerdur Steinthorsdottir, Gudmar Thorleifsson, Augustine Kong, Gunnar Sigurðsson, Unnur Thorsteinsdottir, and Kari Stefansson are employed by deCODE 4 Genetics/Amgen inc.

Mark I McCarthy sits on Advisory Panels for Pfizer and NovoNordisk, has received honoraria from Pfizer NovoNordisk and EliLilly, and is also a recipient of research funding from Pfizer, NovoNordisk, EliLilly, Takeda, Sanofi-Aventis, Merck, Boehringer-Ingelheim, Astra Zeneca, Janssen, Roche, Servier and Abbvie.

Robert A Scott, Laura J Scott, Reedik Mägi, Letizia Marullo, Kyle J Gaulton, Marika Kaakinen, Natalia Pervjakova, Tune H Pers, Andrew D Johnson, John D Eicher, Anne U Jackson, Teresa Ferreira, Yeji Lee, Clement Ma, Lu Qi, Natalie R Van Zuydam, Anubha Mahajan, Han Chen, Peter Almgren, Ben F Voight, Harald Grallert, Martina Müller-Nurasyid, Janina S Ried, N William Rayner, Neil Robertson, Lennart C Karssen, Elisabeth M van Leeuwen, Sara M Willems, Christian Fuchsberger, Phoenix Kwan, Tanya M Teslovich, Pritam Chanda, Man Li , Yingchang Lu, Christian Dina, Dorothee Thuillier, Loic Yengo, Longda Jiang, Thomas Sparso, Hans Kestler, Himanshu Chheda, Lewin Eisele, Stefan Gustafsson, Mattias Frånberg, Rona J Strawbridge, Rafn Benediktsson, Astradur B Hreidarsson, Nicola D Kerrison, Jian'an Luan, Liming Liang, Thomas Meitinger, Michael Roden, Barbara Thorand, Tõnu Esko, Evelin Mihailov, Caroline Fox, Ching-Ti Liu, Denis Rybin, Bo Isomaa, Valeriya Lyssenko, Tiinamaija Tuomi, David J Couper, James S Pankow, Niels Grarup, Christian T Have, Marit E Jørgensen, Torben Jørgensen, Allan Linneberg, Marilyn C Cornelis, Rob M van Dam, David J Hunter, Peter Kraft, Qi Sun, Sarah Edkins, Katharine R Owen, John RB Perry, Andrew R Wood, Eleftheria Zeggini, Juan Tajes-Fernandes, Goncalo R Abecasis, Lori L Bonnycastle, Peter S Chines, Heather M Stringham, Heikki A Koistinen, Leena Kinnunen, Bengt Sennblad, Thomas W Mühleisen, Markus M Nöthen, Sonali Pechlivanis, Damiano Baldassarre, Karl Gertow, Steve E Humphries, Elena Tremoli, Norman Klopp, Julia Meyer, Gerald Steinbach, Roman Wennauer, Johan G Eriksson, Satu Männistö, Leena Peltonen, Emmi Tikkanen, Guillaume Charpentier, Elodie Eury, Stéphane Lobbens, Bruna Gigante, Karin Leander, Olga McLeod, Erwin P Bottinger, Omri Gottesman, Douglas Ruderfer, Matthias Blüher, Peter Kovacs, Anke Tonjes, Nisa M Maruthur, Chiara Scapoli, Raimund Erbel, Karl-Heinz Jöckel, Susanne Moebus, Ulf de Faire, Anders Hamsten, Michael Stumvoll, Panagiotis Deloukas, Peter J Donnelly, Timothy M Frayling, Andrew T Hattersley, Samuli Ripatti, Veikko Salomaa, Nancy L Pedersen, Bernhard O Boehm, Richard N Bergman, Francis S Collins, Karen L Mohlke, Jaakko Tuomilehto, Torben Hansen, Oluf Pedersen, Lars Lannfelt, Erik Ingelsson, Lars Lind, Cecilia M Lindgren, Stephane Cauchi, Philippe Froguel, Ruth JF Loos, Beverley Balkau, Heiner Boeing, Paul W Franks, Aurelio Barricarte Gurrea, Domenico Palli, Yvonne T van der

Schouw, David Altshuler, Leif C Groop, Claudia Langenberg, Nicholas J Wareham, Eric Sijbrands, Cornelia M van Duijn, James B Meigs, Eric Boerwinkle, Christian Gieger, Konstantin Strauch, Andres Metspalu, Andrew D Morris, Colin NA Palmer, Frank B Hu, Josée Dupuis, Andrew P Morris, Michael Boehnke, and Inga Prokopenko declare to have no competing financial interest.

**Table 1. Novel loci associated with T2D from the combination of 1000G-imputed GWAS meta-analysis (stage 1) and Metabochip follow-up (stage 2).**

| | Stage 1 | | | | | | Stage 2 | | | | | | | Stage1+Stage2 | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Locus name*** | **Chr:Position** | **SNV†** | **EA/ NEA** | **EAF** | **OR (CI 95%)** | ***P*-value** | **Chr:Position** | **SNV‡** | **$r^2$ with lead SNV** | **EA/ NEA** | **EAF** | **OR (95% CI)** | ***P*-value** | **OR (95% CI) ¢** | ***P*-value** |
| *ACSL1* | 4:185708807 | rs60780116 | T/C | 0.84 | 1.09 (1.06-1.13) | $7.38x10^{-8}$ | 4:185714289 | rs1996546 | 0.62 | G/T | 0.86 | 1.08 (1.03-1.13) | $5.60x10^{-4}$ | 1.09 (1.06-1.12) | $1.98x10^{-10}$ |
| *HLA-DQA1* | 6:32594309 | rs9271774 | C/A | 0.74 | 1.10 (1.06-1.14) | $3.30x10^{-7}$ | 6:32594328 | rs9271775 | 0.91 | T/C | 0.80 | 1.08 (1.03-1.13) | $7.59x10^{-4}$ | 1.09 (1.06-1.12) | $1.11x10^{-9}$ |
| *SLC35D3* | 6:137287702 | rs6918311 | A/G | 0.53 | 1.07 (1.04-1.10) | $6.67x10^{-7}$ | 6:137299152 | rs4407733 | 0.92 | A/G | 0.52 | 1.05 (1.02-1.08) | $1.63x10^{-3}$ | 1.06 (1.04-1.08) | $6.78x10^{-9}$ |
| *MNX1* | 7:157027753 | rs1182436 | C/T | 0.80 | 1.08 (1.05-1.12) | $8.30x10^{-7}$ | 7:157031407 | rs1182397 | 0.92 | G/T | 0.85 | 1.06 (1.02-1.11) | $4.38x10^{-3}$ | 1.08 (1.05-1.10) | $1.71x10^{-8}$ |
| *ABO* | 9:136155000 | rs635634 | T/C | 0.18 | 1.08 (1.05-1.12) | $3.59x10^{-7}$ | 9:136154867 | rs495828 | 0.83 | T/G | 0.20 | 1.06 (1.01-1.10) | $1.23x10^{-2}$ | 1.08 (1.05-1.10) | $2.30x10^{-8}$ |
| *PLEKHA1* | 10:124186714 | rs2292626 | C/T | 0.50 | 1.09 (1.06-1.11) | $1.75x10^{-12}$ | 10:124167512 | rs2421016 | 0.99 | C/T | 0.50 | 1.05 (1.02-1.08) | $2.30x10^{-3}$ | 1.07 (1.05-1.09) | $1.51x10^{-13}$ |
| *HSD17B12* | 11:43877934 | rs1061810 | A/C | 0.28 | 1.08 (1.05-1.11) | $5.29x10^{-9}$ | 11:43876435 | rs3736505 | 0.92 | G/A | 0.30 | 1.05 (1.01-1.08) | $4.82x10^{-3}$ | 1.07 (1.05-1.09) | $3.95x10^{-10}$ |
| *MAP3K11* | 11:65364385 | rs111669836 | A/T | 0.25 | 1.07 (1.04-1.10) | $7.43x10^{-7}$ | 11:65365171 | rs11227234 | 1.00 | T/G | 0.24 | 1.05 (1.01-1.08) | $8.77x10^{-3}$ | 1.06 (1.04-1.09) | $4.12x10^{-8}$ |
| *NRXN3* | 14:79945162 | rs10146997 | G/A | 0.21 | 1.07 (1.04-1.10) | $4.59x10^{-6}$ | 14:79939993 | rs17109256 | 0.98 | A/G | 0.21 | 1.07 (1.03-1.11) | $1.27x10^{-4}$ | 1.07 (1.05-1.09) | $2.27x10^{-9}$ |
| *CMIP* | 16:81534790 | rs2925979 | T/C | 0.30 | 1.08 (1.05-1.10) | $2.72x10^{-8}$ | 16:81534790 | rs2925979 | 1.00 | T/C | 0.31 | 1.05 (1.02-1.08) | $3.06x10^{-3}$ | 1.07 (1.04-1.09) | $2.27x10^{-9}$ |
| *ZZEF1* | 17:4014384 | rs7224685 | T/G | 0.30 | 1.07 (1.04-1.10) | $2.00x10^{-7}$ | 17:3985864 | rs8068804 | 0.95 | A/G | 0.31 | 1.07 (1.03-1.11) | $4.11x10^{-4}$ | 1.07 (1.05-1.09) | $3.23x10^{-10}$ |
| *GLP2R* | 17:9780387 | rs78761021 | G/A | 0.34 | 1.07 (1.05-1.10) | $5.49x10^{-8}$ | 17:9791375 | rs17676067 | 0.87 | C/T | 0.31 | 1.03 (1.00-1.07) | $3.54x10^{-2}$ | 1.06 (1.04-1.08) | $3.04x10^{-8}$ |
| *GIP* | 17:46967038 | rs79349575 | A/T | 0.51 | 1.07 (1.04-1.09) | $2.61x10^{-7}$ | 17:47005193 | rs15563 | 0.78 | G/A | 0.54 | 1.04 (1.01-1.07) | $2.09x10^{-2}$ | 1.06 (1.03-1.08) | $4.43x10^{-8}$ |

*The nearest gene is listed; this does not imply this is the biologically relevant gene; †Lead SNV types: all map outside transcripts except rs429358 (missense variant) and rs1061810 (3'UTR); ‡Stage 2: proxy SNV ($r^2$>0.6 with stage 1 lead SNV) was used when no stage 1 SNV was available. ¢The meta-analysis OR is aligned to the Stage 1 SNV risk allele. Abbreviations: Chr – chromosome, CI – confidence interval, EA - effect allele, EAF – effect allele frequency, OR – odds ratio, NEA – non-effect allele.